

Amendments to the Claims

The Listing of Claims presented below will replace all prior versions, and listings, of claims in the application.

Listing of Claims

1. A mixture or set of sub-mixtures comprising X-mer precursors,
 - wherein the X-mer precursors have a minimum length of 3 nucleotides;
 - wherein the mixture has a minimum mixture coverage complexity of at least $56/N$ or wherein the set of sub-mixtures has a composite mixture coverage complexity of at least $56/N$, wherein N represents the number of distinct X-mer precursors in the mixture;
 - wherein each sub-mixture in said set has a reduced mixture coverage complexity as compared with the composite mixture coverage complexity;
 - wherein each sub-mixture comprises a plurality of X-mer precursors;
 - wherein said length is selected independently for each X-mer precursor; and
 - wherein the mixture or set of sub-mixtures further comprises a set of tags wherein each tag is covalently linked to at least one X-mer precursor through a cleavable linker.
2. A mixture or set of sub-mixtures comprising X-mer precursors,
 - wherein said X-mer precursors have a minimum length of 3 nucleotides;
 - wherein said mixture has a minimum mixture coverage complexity of at least $56/N$ or wherein said set of sub-mixtures has a composite mixture coverage complexity of at least $56/N$, wherein N represents the number of distinct X-mer precursors in the mixture;
 - wherein each sub-mixture in said set has a reduced mixture coverage complexity as compared with the composite mixture coverage complexity;
 - wherein each sub-mixture further comprises a plurality of X-mer precursors;
 - wherein said length is selected independently for each X-mer precursor;

wherein the mixture or set of sub-mixtures further comprises a set of tags wherein each tag is covalently linked to at least one X-mer precursor through a cleavable linker; and

wherein said X-mer precursors have a determined isotopic composition.

3. The mixture or set of sub-mixtures of claim 1 or 2 wherein said mixture has a mixture coverage complexity of at least about $1/2$ when said mixture contains at least 128 discrete X-mers, or wherein said set of sub-mixtures has a composite mixture coverage complexity of at least about $1/2$ when said set of sub-mixtures contains at least 128 discrete X-mers.
4. The mixture or set of sub-mixtures of claim 1 or 2, wherein said mixture has a mixture coverage complexity of at least about $1/4$ when said mixture contains at least 256 discrete X-mers, or wherein said set of sub-mixtures has a composite mixture coverage complexity of at least about $1/4$ when said set of sub-mixtures contains at least 256 discrete X-mers.
5. The mixture or set of sub-mixtures of claim 1 or 2, wherein said mixture has a mixture coverage complexity of at least about $1/8$ when said mixture contains at least 512 discrete X-mers, or wherein said set of sub-mixtures has a composite mixture coverage complexity of at least about $1/8$ when said set of sub-mixtures contains at least 512 discrete X-mers.
6. The mixture or set of sub-mixtures of claim 1 or 2, wherein nucleotide sequences of the precursors of said mixture or set of sub-mixtures are known.
7. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is between approximately 10-100,000.

8. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is between approximately 20-20,000.
9. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is between approximately 20-10,000.
10. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is between approximately 20-5,000.
11. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is between approximately 50-1000.
12. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is greater than a mass number complexity (MNC) of a natural equivalent of the mixture or set of sub-mixtures, wherein the natural equivalent of the X-mer precursors are extended by one nucleotide, and wherein the number of tags in the set of tags is less than or equal to a number of X-mer precursors in the mixture or set of sub-mixtures.
13. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is greater than 75% of a mass number complexity (MNC) of a natural equivalent of mixture or set of sub-mixtures, wherein the natural equivalent of the X-mer precursors are extended by one nucleotide, and wherein the number of tags in the set of tags is less than or equal to a number of X-mer precursors in the mixture or set of sub-mixtures.

14. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is at least 0.5% of a number of X-mer precursors in the mixture or set of sub-mixtures, and less than or equal to the number of X-mer precursors in the mixture or set of sub-mixtures.
15. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is at least 1% of a number of X-mer precursors in the mixture or set of sub-mixtures, and less than or equal to the number of X-mer precursors in the mixture or set of sub-mixtures.
16. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is at least 10% of a number of X-mer precursors in the mixture or set of sub-mixtures, and less than or equal to the number of X-mer precursors in the mixture or set of sub-mixtures.
17. The mixture or set of sub-mixtures of claim 1 or 2, wherein a number of tags in the set of tags distinguishable by mass spectrometry after cleavage of the linkers is at least 25% of a number of X-mer precursors in the mixture or set of sub-mixtures, and less than or equal to the number of X-mer precursors in the mixture or set of sub-mixtures.
- 18-73. (Cancelled)
74. A kit for carrying out a method of analyzing a target nucleic acid sequence, comprising:
 - a. the mixture or the set of sub-mixtures of claim 1; and
 - b. an enzyme having a nucleotide polymerase activity.

75. The kit of claim 74, further comprising a multiplicity of nucleotides selected from the group consisting of natural chain-terminating triphosphates and modified chain-terminating triphosphates.
76. The kit of claim 74, further comprising chain-terminating nucleotides with an affinity label for purification of nucleic acids.
77. A kit for carrying out a method of analyzing a target nucleic acid sequence comprising:
- the mixture or the set of sub-mixtures of claim 1; and
 - a DNA ligase.
78. A kit for carrying a method of analyzing a target nucleic acid sequence, comprising:
- the mixture or the set of sub-mixtures of claim 1; and
 - a condensing agent.
79. A kit for carrying out a method of analyzing a target nucleic acid sequence having a 3'-end and a 5'-end, comprising:
- the mixture or the set of sub-mixtures of claim 1;
 - a DNA ligase; and
 - an array comprising:
 - a surface; and
 - a multiplicity of nucleic acid sequence probes comprising:
 - a nucleic acid attached to said surface, wherein the nucleic acid has a terminal 3'-hydroxyl end and wherein the 5' end is directly or indirectly attached to said surface.
80. A kit for carrying out a method of analyzing a target nucleic acid sequence having a 3'-end and a 5'-end, comprising:
- the mixture or the set of sub-mixtures of claim 1;
 - a condensing agent; and
 - an array comprising:

- (a) a surface; and
- (b) a multiplicity of nucleic acid sequence probes comprising:
 - (i) a nucleic acid attached to said surface, wherein the nucleic acid has a terminal 3'-hydroxyl end and wherein the 5' end is directly or indirectly attached to said surface.